Average Nucleotide Identity (ANI)

Introduction

Average Nucleotide Identity (ANI) is a measure of nucleotide-level genomic similarity between the coding regions of two genomes. First, BBHs between a genome pair are computed as pairwise bidirectional best nSimScan hits of genes having 70% or more identity and at least 70% coverage of the shorter gene.

Alignment Fraction (AF) is computed using to the following formula:

Average Nucleotide Identity (ANI) is computed using the following formula:

$$\mathbf{gAN} = \frac{\sum_{bbh} (Percent Identity * Alignment length)}{lengths of BBH genes}$$

Pairwise ANI

BBHs between a genome pair are computed as pairwise bidirectional best nSimScan hits of genes having 70% or more identity and at least 70% coverage of the shorter gene. Genome(s) can either be selected from IMG or uploaded as a nucleotide sequence in FASTA format (using the <u>Upload File</u> button) to compute ANI to selected genome(s) in IMG.

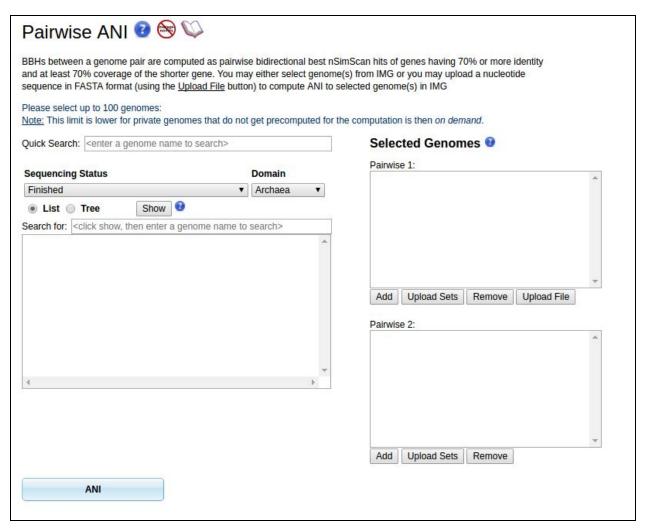


Figure 1. ANI Pairwise

Pairwise ANI is precomputed for most genomes. Private genomes and newly added genomes will be precomputed on-demand which will slow down the computation (Fig. 1b).



Figure 1b. Pairwise ANI - results

Same Species Plot

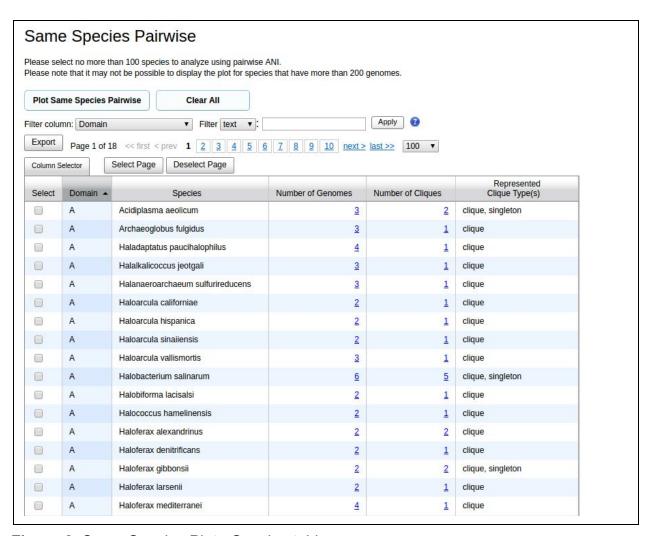


Figure 2. Same Species Plot - Species table

Selecting in the Species table under "Number of Genomes" for a species links to the "Genomes for Species" page (Fig. 2b). Selecting "Number of Cliques" for a species links to the "Cliques for Species" page (Fig. 2c).

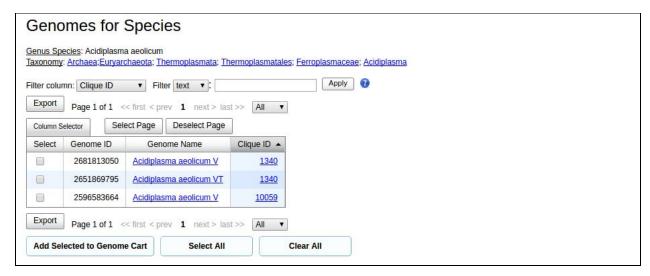


Figure 2b. Genomes for Species

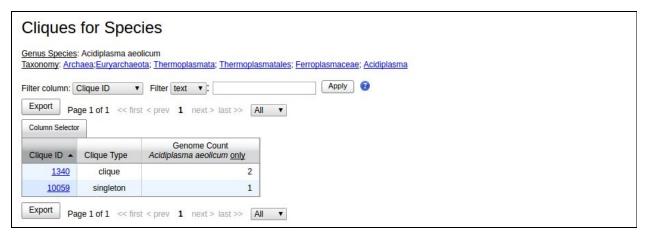


Figure 2c. Cliques for Species

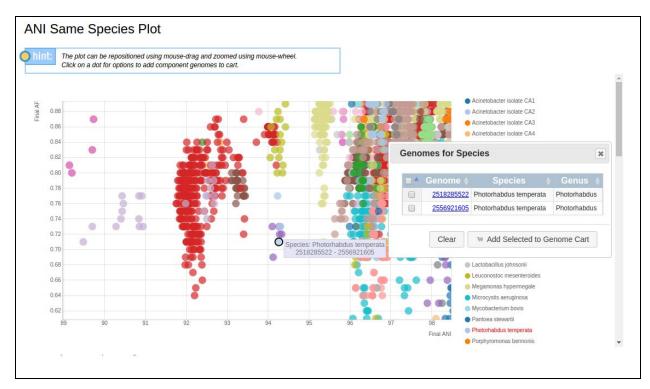


Figure 2d. Same Species Plot

Each dot in the Same Species Plot represents the final ANI vs. final AF for a genome pair present in a given species. Selecting a dot will bring up a dialog box with a table to which the 2 genomes represented in the dot will be added. These genomes can then be reviewed and added to a genome cart.

ANI Cliques

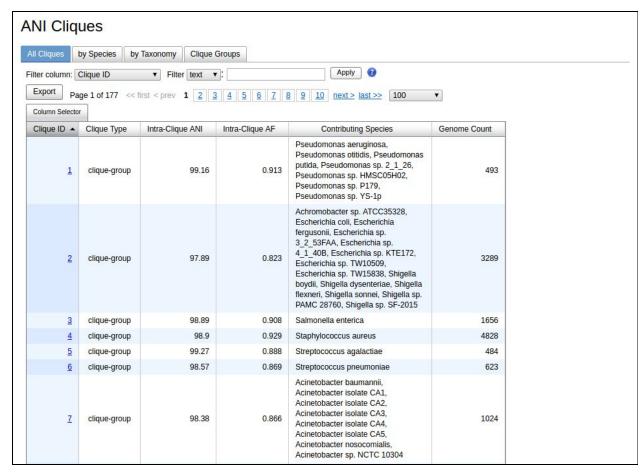


Figure 3. ANI Cliques - by clique ID

Clicking on the clique id in the All Cliques tab will link to the details page for that clique (Fig. 4).

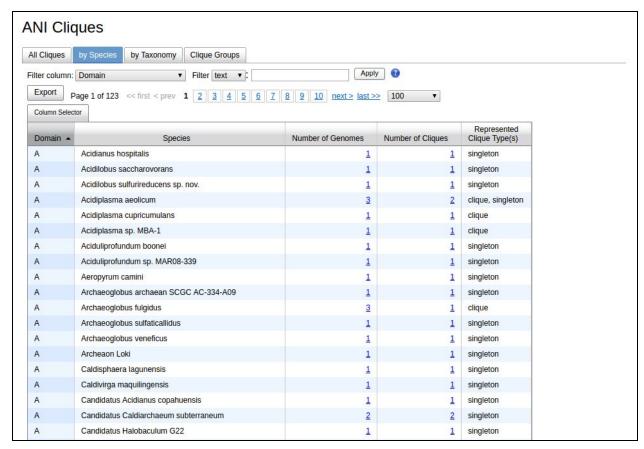


Figure 3b. ANI Cliques by Species

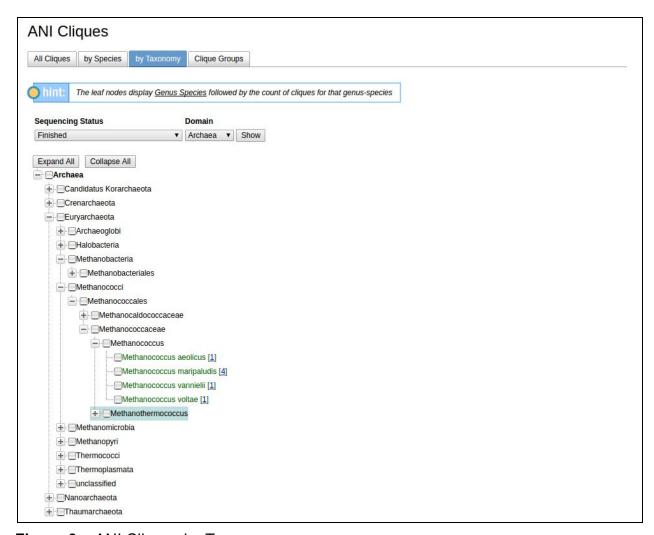


Figure 3c. ANI Cliques by Taxonomy

The leaf nodes in the Taxonomy tree display the <u>Genus Species</u> followed by the count of cliques for that genus-species. Clicking on the count links to the Genus Species detail page. The first tab of this page lists the cliques for this Species (Fig. 3d), while the second tab lists the genomes in that Species (Fig. 3f).



Figure 3d. Genus Species Detail page - Cliques for Species

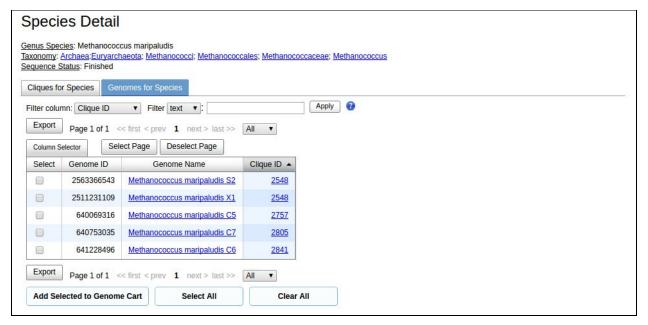


Figure 3f. Genus Species Detail page - Genomes for Species

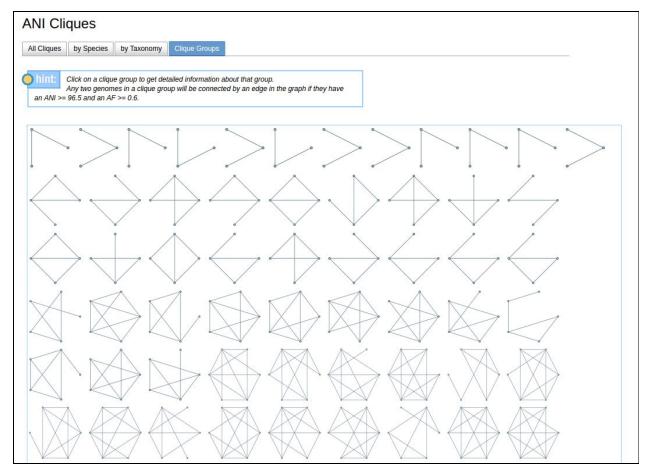


Figure 3g. ANI Cliques - Clique Groups

Any two genomes in a clique group will be connected by an edge in the graph if they have an ANI \geq 96.5 and an AF \geq 0.6. Clicking on the clique graph representation links to details page for that clique group (Fig. 4).

Clique Details



Figure 4. Clique Details - Overview

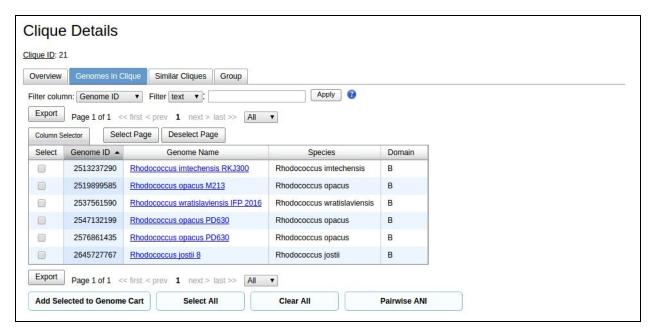


Figure 4b. Clique Details - Genomes in Clique

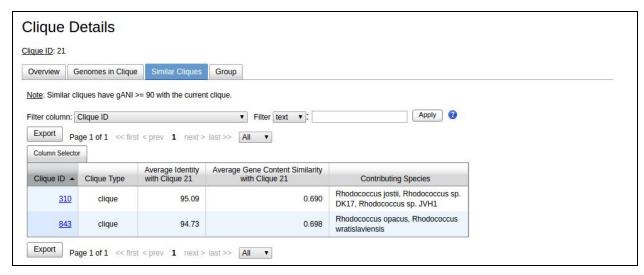


Figure 4c. Clique Details - Similar Cliques

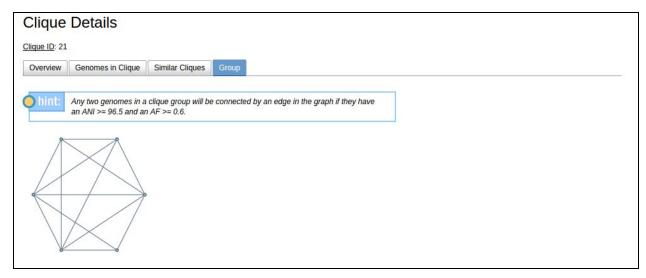


Figure 4d. Clique Details - Clique Group

Genome Detail Page

ANI information for a particular genome can be found on the genome detail page, located to the right of Genome Statistics.

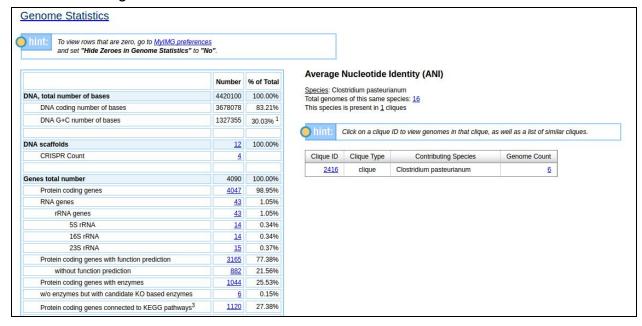


Figure 5. Genome Detail - ANI